

Scientific & technical services for the sampling of reference genomes of eukaryotic species from biodiversity hotspots in Croatia

We are searching for tenders that can perform field campaigns aiming at collecting as many species as possible in a specific area over a short period (hereafter referred to as Bioblitz expedition) in biodiversity hotspots within Croatia and concretely cave systems in the Dinarides, a hotspot for cave biodiversity. The goal is to collect at least one representative for each of the major cave invertebrate groups that can be submitted for full genome sequencing and/or reference barcode generation. These groups are: sponges, hydrozoans, flatworms, gastropods, bivalves, opiliones, spiders, pseudoscorpiones, palpigrades, diplopods, chilopods, terrestrial and aquatic isopods, amphipods, decapods, collembolans, diplurans, orthopterans, cixiids, and coleopterans. Special priority should be given to species whose genomes are not being sequenced as part of other biodiversity genomics initiatives (as verified on the web server Genomes on a Tree, [GoaT](#)). The collection campaigns and the full project need to be carried out during 2024.

All campaigns should be accompanied by reported citizen science activities related to the topic.

Services offered must include:

- Species collection with associated metadata (eg, location, time of collection, team members, type of tissue, etc).
- Taxonomic identification for all the species collected for genome sequencing and barcoding.
- Preservation of fresh specimen samples suitable for reference genome sequencing (e.g., dry ice, liquid nitrogen, or similar) and DNA barcoding, vouchers and biobanking (e.g., 96% ethanol)
- Permission clearance for field collection, sample export to Spain, Nagoya permits if necessary, and all permits that may apply following the local and national regulations; and
- Shipment of samples to the designated coordination hub (Institute of Evolutionary Biology, CSIC, Barcelona, Spain).

Guidelines on how the samples need to be collected and stored to ensure good preservation of the specimen samples for reference genome sequencing, vouchers, biobanking, and barcoding will be provided before the start of the project.

Requirements of applicant Companies/Institutions:

- Applicants must be ERGA members. Those who are interested but are not yet members are encouraged to join ERGA before the application deadline in order to be considered. Information about how to do it can be found [here](#).
- BGE project partners and their affiliated entities are not eligible to apply. A list of all official partners can be checked [here](#).
- Applicants should be located in the same country/geographical area where the BioBlitz expeditions are proposed. Applicants should comply with all the local and EU regulations. Applications of collaborative nature if the incentive of capacity building in the country of sample origin are encouraged, although one single Institution must act as contractor.
- All the samples must be shipped to the coordination hub in Barcelona before the 30th of October 2024, and the project should be completed by the 31st of December 2024.
- Applicants are required to obtain all necessary collection, ethical, and Nagoya permits for each species they intend to collect. These permits must be submitted to the coordination hub at the project's outset. The same applies to export permits to Spain (the country where the coordination hub is located), as well as a Material Transfer Agreement (MTA) between the applicant's institution and the coordination hub. Applicants are responsible for adhering to national and regional wildlife regulations. Therefore, it is imperative that they consult the relevant national/regional authorities to determine the specific permits required for sample collection at each location and for each species. Protected specimens will not be collected unless with explicit permission and justification.
- Applicants should adhere to the open data and FAIR principles according to EU policy (<https://pro.europeana.eu/post/europeana-and-the-fair-principles-for-research-data>), to the BGE [Sampling Code of Practice](#) guidelines, and to the BGE data management plan (to be shared with the applicants upon start of the project). Applicants will retain no intellectual property (IP) rights to the results generated by the project; such rights will primarily remain with the project beneficiaries. Specific IP arrangements, including conditions under which IP rights are shared with subcontractors, will be addressed in subcontracting agreements. These agreements will ensure alignment with overarching project and EU regulations, clarifying the sharing of IP rights among project beneficiaries and subcontractors.
- Applicants should collect a minimum number of 150 species, with enough samples per species for obtaining a reference genome, vouchering, biobanking and barcoding. Further instructions on sample collection will be shared before the beginning of the project.